Amendments to the Specification

Please replace the paragraph beginning at page 4, line 13, with the following rewritten paragraph:

The method of the present invention also includes inducing apoptosis in a target cell by inhibiting a cell fate determining function of a Notch protein in the target cell at a time when the cell is undergoing differentiation, further comprising treating the target cell with a therapeutically effective amount of another antineoplastic agent at a time that enhances apoptosis in the target cell. The other antineoplastic agent includes for example vinca alkaloids, for example vinblastine, Paclitaxel and vincristine. The antineoplastic agent can also be administered substantially ~~concurruently~~ concurrently with the agent administered to inhibit a cell fate determining function of a Notch protein in the target cell at a time when the cell is undergoing differentiation, which induces the target cell to undergo apoptosis. In a further embodiment, a method of inducing apoptosis in a tumor cell that is characterized by increased expression of a Notch protein by administering a therapeutically effective amount of a first antineoplasic agent to a subject having a tumor and interfering with the Notch function or expression in the cells of the tumor, at a time during differentiation when the Notch is required to prevent apoptosis, by administering a molecule that specifically interferes with the Notch function or expression at a time that enhances an effect of the first antineoplastic agent. The first antineoplastic agent which ~~interfers~~ interferes with the Notch function or expression can include a Notch antisense oligonucleotide that specifically blocks expression of the Notch protein or an antibody which specifically binds to the Notch protein and interferes with Notch function. The tumor can be selected from the group consisting of cervical cancer, breast cancer, colon cancer, melanoma, seminoma, lung cancer, and hematopoietic malignancy.

Please replace the paragraph beginning at page 14, line 27, with the following rewritten paragraph:

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al., *J. Mol. Biol.* 215:403-410, 1990) is available from several sources, including the National Center for Biological Information (NBCI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. [[It can be accessed at

http://www.ncbi.nlm.nih.gov/BLAST/. A description of how to determine sequence identity using this program is available at http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html.]]

Please replace the paragraph beginning at page 15, line 1, with the following rewritten paragraph:

Homologs of the Notch proteins are typically characterized by possession of at least 70% sequence identity counted over the full length alignment with the disclosed amino acid sequence using the NCBI Blast 2.0, gapped blastp set to default parameters. Such homologous peptides will more preferably possess at least 75%, more preferably at least 80% and still more preferably at least 90% or 95% sequence identity determined by this method. When less than the entire sequence is being compared for sequence identity, homologs will possess at least 75% and more preferably at least 85% and more preferably still at least 90% or 95% sequence identity over short windows of 10-20 amino acids. [[Methods for determining sequence identity over such short windows are described at http://www.ncbi.nlm.nih.gov/BLAST/blast_FAQs.html.]] One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs or other variants could be obtained that fall outside of the ranges provided.